AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraphs on page 3, line 6 – page 4, line 2 as follows:

Accordingly, in its first aspect the present invention relates to an enzyme exhibiting endo-β-1,4-glucanase activity (EC 3.2.1.4) which is selected from one of (a) a polypeptide encoded by the DNA sequence of positions 76 to 1455 of SEQ ID NO: 1; (b) a polypeptide produced by culturing a cell comprising the sequence of SEQ ID NO: 1 under conditions wherein the DNA sequence is expressed; (c) an endo-β-1,4-glucanase enzyme having a sequence of at least 75% identity to positions ~~26-485~~ 1-456 of SEQ ID NO: 2 polypeptide comprising an amino acid sequence derived from the amino acid sequence of positions ~~26-485~~ 1-456 of SEQ ID NO: 2 when identity is determined by GAP provided in the GCG program package using a GAP creation penalty of 3.0 and GAP extension penalty of 0.1; and (d) a polypeptide encoded by the endoglucanase encoding part of the DNA sequence obtainable from the plasmid in *Escherichia coli* DSM 12805. The enzyme of the invention is identified as belonging to family 9 of glycosyl hydrolases as defined by Henrissat et al.

In its second aspect the invention relates to an isolated polynucleotide molecule, preferably a DNA molecule, encoding the catalytically active domain of an enzyme exhibiting endo-β-1,4-glucanase activity which molecule is selected from the group consisting of (a) polynucleotide molecules comprising a nucleotide sequence as shown in SEQ ID NO: 1 from nucleotide 76 to nucleotide 1455, (b) species homologs of (a); (c) polynucleotide molecules that encode a polypeptide that is at least 75% identical to the amino acid sequence of SEQ ID NO: 2 from amino acid residue ~~26~~ 1 to amino acid residue 456 ~~485~~, and (c) degenerate nucleotide sequences of (a) or (b); preferably a polynucleotide molecule capable of hybridizing to a denatured double-stranded DNA probe under medium stringency conditions, wherein the probe is selected from the group consisting of DNA probes comprising the sequence shown in positions 76-1455 of SEQ ID NO: 1 and DNA probes comprising a sub-sequence of positions 76-1455 of SEQ ID NO: 1 having a length of at least about 100 base pairs.

Please amend the paragraphs on page 11, lines 5-33 as follows:

The sequence of amino acids in position ~~26~~ 1 to about position ~~485~~ 456 of SEQ ID NO: 2 is a mature endoglucanase sequence of the catalytic active domain. The enzyme further comprises a cellulose binding domain (CBD) which is operably linked to the catalytic active domain and

which is represented by an amino acid sequence corresponding to from about position ~~485~~ 457 to position ~~646~~ 617 of SEQ ID NO: 2. The CBD of the present endoglucanase belongs to family 3b, cf. below.

The present invention also provides endoglucanase polypeptides that are substantially homologous to the polypeptide of SEQ ID NO: 2 and species homologs (paralogs or orthologs) thereof. The term "substantially homologous" is used herein to denote polypeptides having 75%, preferably at least 80%, more preferably at least 85%, and even more preferably at least 90%, sequence identity to the sequence shown in amino acids nos. ~~26-485~~ 1-456 or nos. ~~26-646~~ 1-617 of SEQ ID NO: 2 or their orthologs or paralogs. Such polypeptides will more preferably be at least 95% identical, and most preferably 98% or more identical to the sequence shown in amino acids nos. ~~26-646~~ 1-617 of SEQ ID NO: 2 or its orthologs or paralogs. Percent sequence identity is determined by conventional methods, by means of computer programs known in the art such as GAP provided in the GCG program package (Program Manual for the Wisconsin Package, Version 8, August 1994, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711) as disclosed in Needleman, S.B. and Wunsch, C.D., (1970), Journal of Molecular Biology, 48, 443-453, which is hereby incorporated by reference in its entirety. GAP is used with the following settings for polypeptide sequence comparison: GAP creation penalty of 3.0 and GAP extension penalty of 0.1.

Please amend the paragraph on page 14, lines 28-32 as follows:

Using the methods discussed above, one of ordinary skill in the art can identify and/or prepare a variety of polypeptides that are substantially homologous to residues ~~26~~ 1 to about 485 456 or residues ~~26~~ 1 to ~~646~~ 617 of SEQ ID NO: 2 and retain the endoglucanase activity of the wild-type protein.

Please amend the paragraph on page 31, lines 23-30 as follows:

The plasmid from MB905 was introduced to a derivative of *B. licheniformis* ATCC 14580, for expression trials. This strain was termed MB924. The cloned DNA sequence was expressed in *B. licheniformis* by fermenting the cells in BP-X media at 37°C for 5 days at 300 rpm. The endoglucanase protein that appeared in the supernatant corresponded to the mature protein of

SEQ ID NO: 2, i.e. comprisinged the protein sequence corresponding to the of amino acids at positions 26-646 1-617 of SEQ ID NO: 2.

Please amend the paragraph on page 32, line 37 – page 33, line 5 as follows:

The pure endoglucanase comprises a catalytic domain belonging to family 9 of glycosyl hydrolases, which domain corresponds to the amino acid sequence from about position 26-1 to about position 485-456 of SEQ ID NO: 2, and a cellulase binding domain (CBD) which is linked to the catalytic domain and is represented by the the amino acid sequence from about position 486 457 to position 644-617 of SEQ ID NO: 2. The CBD belongs to family 3b.